X-15648.ST25.txt
SEQUENCE LISTING

<110> Beals, John
      Kuchibhotla, Uma

<120> HETEROLOGOUS G-CSF FUSION PROTEINS

<130> X-15648

<150> PCT/US03/03120
<151> 2003-02-21

<160> 66

<170> PatentIn version 3.2

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cagaattccg tggaacgggt cggg                                            1044
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cgtcgcgagg tcgagaagct gtgtaacacc accaagctgt gccaccccga ggagctggtg    240

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acccagggtg ccatgccggc cttcgcctct gctttccggg acgtcgggtg ggtcccacgg    840

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caactccata gcgggtcgtt gcggtgggtc gaccgtccga cgaactcggt tgaggtatcg    480

ggccttttcc tctaccaggg gctcctgcag gccctggaag ggatctcccc ggaaaaggag    540

atggtccccg aggacgtccg ggaccttccc tagaggcccg agttgggtcc caccttggac    600

acactgcagc tggacgtcgc cgacgggctc aacccagggt ggaacctgtg tgacgtcgac    660

ctgcagcggc tgtttgccac caccatctgg cagcagatgg aagaactggg aatggcccct    720

aaacggtggt ggtagaccgt cgtctacctt cttgaccctt accggggagc cctgcagccc    780

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tctctgggca tcccctgggc tcccctgagc agctgcgacg agcctgtgac agacccgtag     360

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ctggaggtgt cgtaccgcgt cttaaggcac cttgcccagc ccgacctcca cagcatggcg    1020

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<213>   Artificial Sequence

<220>
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Page 12

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cagggcgatg gcgcagcgct ccagcggaat ctcgttcact ccttctaggt cccgctaccg    180

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caactccata gcgggtcgtt gcggtgggtc gaccgtccga cgaactcggt tgaggtatcg    480

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ctgcagcggc tgtttgccac caccatctgg cagcagatgg aagaactggg aatggcccct    720

aaacggtggt ggtagaccgt cgtctacctt cttgaccctt accggggagc cctgcagccc    780

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ctggaggtgt cgtaccgcgt cttaaggcac cttgcccagc ccgacctcca cagcatggcg   1020

cagaattccg tggaacgggt cggg                                          1044
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<213>  Artificial Sequence

<220>
<223>  synthetic construct

<400>  16
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cgtcgcgagg tcgagaagct gtgtaacacc accaagctgt gccaccccga ggagctggtg    240

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tctctgggca tcccctgggc tcccctgagc aattgcgacg agcctgtgac agacccgtag    360

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caactccata gctggtcggt ccgggacgtc gaccgtccga cgaactcggt tgaggtatcg    480

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acactgcagc tggacgtcgc cgacgggctc aacccagggt ggaacctgtg tgacgtcgac    660

ctgcagcggc tgtttgccac caccatctgg cagcagatgg aagaactggg aatggcccct    720

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<220>
<223>   synthetic construct

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aaattagtga atgaagtaac tgaatttgca aaaacatgtg ttgctgatga gtcagctgaa    180

aattgtgaca atcacttca taccctttttt ggagacaaat tatgcacagt tgcaactctt    240

cgtgaaacct atggtgaaat ggctgactgc tgtgcaaaac aagaacctga gagaaatgaa    300

tgcttcttgc aacacaaaga tgacaaccca aacctccccc gattggtgag accagaggtt    360

gatgtgatgt gcactgcttt tcatgacaat gaagagacat ttttgaaaaa atacttatat    420

gaaattgcca gaagacatcc ttacttttat gccccggaac tccttttctt tgctaaaagg    480

tataaagctg cttttacaga atgttgccaa gctgctgata aagctgcctg cctgttgcca    540

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gccagtctcc aaaaatttgg agaaagagct ttcaaagcat gggcagtagc tcgcctgagc    660

cagagatttc ccaaagctga gtttgcagaa gtttccaagt tagtgacaga tcttaccaaa    720

gtccacacgg aatgctgcca tggagatctg cttgaatgtg ctgatgacag ggcggacctt    780

gccaagtata tctgtgaaaa tcaagattcg atctccagta aactgaagga atgctgtgaa    840

aaacctctgt tggaaaaatc ccactgcatt gccgaagtgg aaaatgatga gatgcctgct    900

gacttgcctt cattagctgc tgattttgtt gaaagtaagg atgtttgcaa aaactatgct    960

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cctgaagcaa aaagaatgcc ctgtgcagaa gactatctat ccgtggtcct gaaccagtta   1380

tgtgtgttgc atgagaaaac gccagtaagt gacagagtca ccaaatgctg cacagaatcc   1440
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Page 14

ttggtgaaca ggcgaccatg cttttcagct ctggaagtcg atgaaacata cgttcccaaa   1500

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agacaaatca gaaacaaac tgcacttgtt gagctcgtga aacacaagcc caaggcaaca   1620

aaagagcaac tgaaagctgt tatggatgat ttcgcagctt ttgtagagaa gtgctgcaag   1680

gctgacgata aggagacctg ctttgccgag gagggtaaaa aacttgttgc tgcaagtcaa   1740

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<213>   Artificial Sequence

<220>
<223>   synthetic construct

<400>   18

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Ala Pro Glu Lys Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro
                20   25   30

Lys Asp Thr Lys Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val
            35   40   45

Val Asp Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val
        50   55   60

Asp Gly Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln
65   70   75   80

Tyr Asn Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln
                85   90   95

Asp Trp Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala
                100   105   110

Leu Pro Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro
            115   120   125

Arg Glu Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr
            130   135   140

Lys Asn Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser
145   150   155   160

Asp Ile Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr
                165   170   175

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Lys Thr Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr
            180             185             190

Ser Lys Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe
            195             200             205

Ser Cys Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys
    210             215             220

Ser Leu Ser Leu Ser Pro Gly Lys
225             230
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<210> 19
<211> 229
<212> PRT
<213> Artificial Sequence

<220>
<223> synthetic contruct

<400> 19

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Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr
            20              25              30

Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val
        35              40              45

Ser Gln Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val
    50              55              60

Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser
65              70              75              80

Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu
            85              90              95

Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser
            100             105             110

Ser Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro
            115             120             125

Gln Val Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln
    130             135             140

Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala
145             150             155             160

Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr
            165             170             175
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Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu
            180   185   190

Thr Val Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser
            195   200   205

Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser
            210   215   220

Leu Ser Leu Gly Lys
225

<210>   20
<211>   585
<212>   PRT
<213>   Artificial Sequence

<220>
<223>   synthetic construct

<400>   20

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1   5   10   15

Glu Asn Phe Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln
            20   25   30

Gln Cys Pro Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu
            35   40   45

Phe Ala Lys Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys
    50   55   60

Ser Leu His Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu
65   70   75   80

Arg Glu Thr Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro
                85   90   95

Glu Arg Asn Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu
            100   105   110

Pro Arg Leu Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His
            115   120   125

Asp Asn Glu Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg
            130   135   140

Arg His Pro Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg
145   150   155   160

Tyr Lys Ala Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala
            165   170   175

Cys Leu Leu Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser
            180   185   190

Ser Ala Lys Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu
            195   200   205

Arg Ala Phe Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro
    210   215   220

Lys Ala Glu Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys
225   230   235   240

Val His Thr Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp
            245   250   255

Arg Ala Asp Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser
            260   265   270

Ser Lys Leu Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His
        275   280   285

Cys Ile Ala Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser
    290   295   300

Leu Ala Ala Asp Phe Val Glu Ser Lys Asp Val Cys Lys Asn Tyr Ala
305   310   315   320

Glu Ala Lys Asp Val Phe Leu Gly Met Phe Leu Tyr Glu Tyr Ala Arg
            325   330   335

Arg His Pro Asp Tyr Ser Val Val Leu Leu Leu Arg Leu Ala Lys Thr
            340   345   350

Tyr Glu Thr Thr Leu Glu Lys Cys Cys Ala Ala Ala Asp Pro His Glu
        355   360   365

Cys Tyr Ala Lys Val Phe Asp Glu Phe Lys Pro Leu Val Glu Glu Pro
    370   375   380

Gln Asn Leu Ile Lys Gln Asn Cys Glu Leu Phe Glu Asn Leu Gly Glu
385   390   395   400

Tyr Lys Phe Gln Asn Ala Leu Leu Val Arg Tyr Thr Lys Lys Val Pro
            405   410   415

Gln Val Ser Thr Pro Thr Leu Val Glu Val Ser Arg Asn Leu Gly Lys
            420   425   430

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Val Gly Ser Lys Cys Cys Lys His Pro Glu Ala Lys Arg Met Pro Cys
        435             440             445

Ala Glu Asp Tyr Leu Ser Val Val Leu Asn Gln Leu Cys Val Leu His
    450             455             460

Glu Lys Thr Pro Val Ser Asp Arg Val Thr Lys Cys Cys Thr Glu Ser
465             470             475             480

Leu Val Asn Arg Arg Pro Cys Phe Ser Ala Leu Glu Val Asp Glu Thr
            485             490             495

Tyr Val Pro Lys Glu Phe Asn Ala Glu Thr Phe Thr Phe His Ala Asp
            500             505             510

Ile Cys Thr Leu Ser Glu Lys Glu Arg Gln Ile Lys Lys Gln Thr Ala
        515             520             525

Leu Val Glu Leu Val Lys His Lys Pro Lys Ala Thr Lys Glu Gln Leu
    530             535             540

Lys Ala Val Met Asp Asp Phe Ala Ala Phe Val Glu Lys Cys Cys Lys
545             550             555             560

Ala Asp Asp Lys Glu Thr Cys Phe Ala Glu Glu Gly Lys Lys Leu Val
            565             570             575

Ala Ala Ser Gln Ala Ala Leu Gly Leu
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<212> DNA
<213> Artificial Sequence

<220>
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<400> 21
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gacatcgccg tggagtggga gagcaatggg cagccggaga acaactacaa gaccacgcct   540
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<210> 22
<211> 981
<212> DNA
<213> Artificial Sequence

<220>
<223> synthetic construct

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aactcaggcg ccctgaccag cggcgtgcac accttcccgg ctgtcctaca gtcctcagga   180

ctctactccc tcagcagcgt ggtgaccgtg ccctccagca gcttgggcac gaagacctac   240

acctgcaacg tagatcacaa gcccagcaac accaaggtgg acaagagagt tgagtccaaa   300

tatggtcccc catgcccacc ctgcccagca cctgagttcc tggggggacc atcagtcttc   360

ctgttccccc caaaacccaa ggacactctc atgatctccc ggacccctga ggtcacgtgc   420

gtggtggtgg acgtgagcca ggaagacccc gaggtccagt tcaactggta cgtggatggc   480

gtggaggtgc ataatgccaa gacaaagccg cgggaggagc agttcaacag cacgtaccgt   540

gtggtcagcg tcctcaccgt cctgcaccag gactggctga cggcaagga gtacaagtgc   600

aaggtctcca acaaaggcct cccgtcctcc atcgagaaaa ccatctccaa agccaaaggg   660

cagccccgag agccacaggt gtacaccctg cccccatccc aggaggagat gaccaagaac   720

caggtcagcc tgacctgcct ggtcaaaggc ttctacccca gcgacatcgc cgtggagtgg   780

gagagcaatg ggcagccgga gaacaactac aagaccacgc ctcccgtgct ggactccgac   840

ggctccttct tcctctacag caggctaacc gtggacaaga gcaggtggca ggagggaat   900

gtcttctcat gctccgtgat gcatgaggct ctgcacaacc actacacaca gaagagcctc   960

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<400> 23

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
1   5   10   15

Ala Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
            20   25   30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
    35   40   45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
    50   55   60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
65   70   75   80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
            85   90   95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
        100   105   110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
        115   120   125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
      130   135   140

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
145   150   155   160

Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Glu Pro
        165   170   175

Lys Ser Cys Asp Lys Thr His Thr Cys Pro Pro Cys Pro Ala Pro Glu
        180   185   190

Leu Leu Gly Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp
      195   200   205

Thr Leu Met Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp
    210   215   220

Val Ser His Glu Asp Pro Glu Val Lys Phe Asn Trp Tyr Val Asp Gly
225   230   235   240

Val Glu Val His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Tyr Asn
        245   250   255

Ser Thr Tyr Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp
        260   265   270

Leu Asn Gly Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Ala Leu Pro
      275   280   285

Ala Pro Ile Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu
    290   295   300

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Pro Gln Val Tyr Thr Leu Pro Pro Ser Arg Glu Glu Met Thr Lys Asn
305                 310             315             320


Gln Val Ser Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile
                325             330             335


Ala Val Glu Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr
                340             345             350


Thr Pro Pro Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Lys
        355             360             365


Leu Thr Val Asp Lys Ser Arg Trp Gln Gln Gly Asn Val Phe Ser Cys
    370             375             380


Ser Val Met His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu
385             390             395             400


Ser Leu Ser Pro Gly Lys
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<210>   24
<211>   403
<212> PRT
<213> Artificial Sequence

<220>
<223>   synthetic construct

<400>   24

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1               5               10              15


Ala Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
            20              25              30


Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
        35              40              45


Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
    50              55              60


Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
65              70              75              80


Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
                85              90              95


Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
            100             105             110


Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
        115             120             125
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Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
    130   135   140

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
145   150   155   160

Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Glu Ser
                165   170   175

Lys Tyr Gly Pro Pro Cys Pro Ser Cys Pro Ala Pro Glu Phe Leu Gly
            180   185   190

Gly Pro Ser Val Phe Leu Phe Pro Pro Lys Pro Lys Asp Thr Leu Met
            195   200   205

Ile Ser Arg Thr Pro Glu Val Thr Cys Val Val Val Asp Val Ser Gln
    210   215   220

Glu Asp Pro Glu Val Gln Phe Asn Trp Tyr Val Asp Gly Val Glu Val
225   230   235   240

His Asn Ala Lys Thr Lys Pro Arg Glu Glu Gln Phe Asn Ser Thr Tyr
            245   250   255

Arg Val Val Ser Val Leu Thr Val Leu His Gln Asp Trp Leu Asn Gly
            260   265   270

Lys Glu Tyr Lys Cys Lys Val Ser Asn Lys Gly Leu Pro Ser Ser Ile
        275   280   285

Glu Lys Thr Ile Ser Lys Ala Lys Gly Gln Pro Arg Glu Pro Gln Val
    290   295   300

Tyr Thr Leu Pro Pro Ser Gln Glu Glu Met Thr Lys Asn Gln Val Ser
305   310   315   320

Leu Thr Cys Leu Val Lys Gly Phe Tyr Pro Ser Asp Ile Ala Val Glu
            325   330   335

Trp Glu Ser Asn Gly Gln Pro Glu Asn Asn Tyr Lys Thr Thr Pro Pro
            340   345   350

Val Leu Asp Ser Asp Gly Ser Phe Phe Leu Tyr Ser Arg Leu Thr Val
            355   360   365

Asp Lys Ser Arg Trp Gln Glu Gly Asn Val Phe Ser Cys Ser Val Met
    370   375   380

His Glu Ala Leu His Asn His Tyr Thr Gln Lys Ser Leu Ser Leu Ser
385   390   395   400

Leu Gly Lys

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<212>   PRT
<213>   Artificial Sequence

<220>
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<400>   25

Thr Pro Leu Gly Pro Ala Ser Ser Leu Pro Gln Ser Phe Leu Leu Lys
1   5   10   15

Ala Leu Glu Gln Val Arg Lys Ile Gln Gly Asp Gly Ala Ala Leu Gln
                20   25   -   30

Glu Lys Leu Cys Ala Thr Tyr Lys Leu Cys His Pro Glu Glu Leu Val
        35   40   45

Leu Leu Gly His Ser Leu Gly Ile Pro Trp Ala Pro Leu Ser Ser Cys
    50   55   60

Pro Ser Gln Ala Leu Gln Leu Ala Gly Cys Leu Ser Gln Leu His Ser
65   70   75   80

Gly Leu Phe Leu Tyr Gln Gly Leu Leu Gln Ala Leu Glu Gly Ile Ser
                85   90   95

Pro Glu Leu Gly Pro Thr Leu Asp Thr Leu Gln Leu Asp Val Ala Asp
                100   105   110

Phe Ala Thr Thr Ile Trp Gln Gln Met Glu Glu Leu Gly Met Ala Pro
        115   120   125

Ala Leu Gln Pro Thr Gln Gly Ala Met Pro Ala Phe Ala Ser Ala Phe
    130   135   140

Gln Arg Arg Ala Gly Gly Val Leu Val Ala Ser His Leu Gln Ser Phe
145   150   155   160

Leu Glu Val Ser Tyr Arg Val Leu Arg His Leu Ala Gln Pro Gly Gly
                165   170   175

Gly Gly Ser Gly Gly Gly Gly Ser Gly Gly Gly Ser Asp Ala His
                180   185   190

Lys Ser Glu Val Ala His Arg Phe Lys Asp Leu Gly Glu Glu Asn Phe
            195   200   205

Lys Ala Leu Val Leu Ile Ala Phe Ala Gln Tyr Leu Gln Gln Cys Pro
210   215   220

Phe Glu Asp His Val Lys Leu Val Asn Glu Val Thr Glu Phe Ala Lys
225   230   235   240

Thr Cys Val Ala Asp Glu Ser Ala Glu Asn Cys Asp Lys Ser Leu His
                245   250   255

Thr Leu Phe Gly Asp Lys Leu Cys Thr Val Ala Thr Leu Arg Glu Thr
                260   265   270

Tyr Gly Glu Met Ala Asp Cys Cys Ala Lys Gln Glu Pro Glu Arg Asn
                275   280   285

Glu Cys Phe Leu Gln His Lys Asp Asp Asn Pro Asn Leu Pro Arg Leu
                290   295   300

Val Arg Pro Glu Val Asp Val Met Cys Thr Ala Phe His Asp Asn Glu
305   310   315   320

Glu Thr Phe Leu Lys Lys Tyr Leu Tyr Glu Ile Ala Arg Arg His Pro
                325   330   335

Tyr Phe Tyr Ala Pro Glu Leu Leu Phe Phe Ala Lys Arg Tyr Lys Ala
                340   345   350

Ala Phe Thr Glu Cys Cys Gln Ala Ala Asp Lys Ala Ala Cys Leu Leu
                355   360   365

Pro Lys Leu Asp Glu Leu Arg Asp Glu Gly Lys Ala Ser Ser Ala Lys
                370   375   380

Gln Arg Leu Lys Cys Ala Ser Leu Gln Lys Phe Gly Glu Arg Ala Phe
385   390   395   400

Lys Ala Trp Ala Val Ala Arg Leu Ser Gln Arg Phe Pro Lys Ala Glu
                405   410   415

Phe Ala Glu Val Ser Lys Leu Val Thr Asp Leu Thr Lys Val His Thr
                420   425   430

Glu Cys Cys His Gly Asp Leu Leu Glu Cys Ala Asp Asp Arg Ala Asp
                435   440   445

Leu Ala Lys Tyr Ile Cys Glu Asn Gln Asp Ser Ile Ser Ser Lys Leu
                450   455   460

Lys Glu Cys Cys Glu Lys Pro Leu Leu Glu Lys Ser His Cys Ile Ala
465   470   475   480

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Glu Val Glu Asn Asp Glu Met Pro Ala Asp Leu Pro Ser Leu Ala Ala
                    485   490   495

Asp Phe Val Glu
                500

<210>   26
<211>   69
<212>   DNA
<213>   Artificial Sequence

<220>
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atgaagctg   69

<210>   27
<211>   61
<212>   DNA
<213>   Artificial Sequence

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g   61

<210>   28
<211>   59
<212>   DNA
<213>   Artificial Sequence

<220>
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<400>   28
ggacagtgca ggaagccact ccactgggcc cagccagctc cctgccccag agcttcctg   59

<210>   29
<211>   72
<212>   DNA
<213>   Artificial Sequence

<220>
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<400>   29
gaacctcgag gatcctcatt agggctgggc aaggtgcctt aagacgcggt acgacacctc   60

caggaagctc tg   72

<210>   30
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<212>   DNA
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<220>

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<400>   30
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atgaagctg   69

<210>   31
<211>   57
<212>   DNA
<213>   Artificial Sequence

<220>
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<210>   32
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<212>   DNA
<213>   Artificial Sequence

<220>
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gggcccagcg agctccctgc cccagagctt cctgctcaag gccttagagc aag   53

<210>   33
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<220>
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caggaagctc tg   72

<210>   34
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<212>   DNA
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atgaagctg   69

<210>   35
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g   61

<210> 36
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gtgctg   66

<210> 37
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<400> 37
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caggaagctc tg   72

<210> 38
<211> 69
<212> DNA
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atgaagctg   69

<210> 39
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<400> 39
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g   61

<210> 40
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caggaagctc tg   72

<210> 42
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<212> DNA
<213> Artificial Sequence

<220>
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atgaagctg   69

<210> 43
<211> 68
<212> DNA
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<220>
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ggggccat   68

<210> 44
<211> 74
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ccagcgccgg gcag   74

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caggaagctc tg   72

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<212>   DNA
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gggcatcgtt aacgctaccc tgagcagctg   30

<210>   49
<211>   27
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<400>   49
gactcgagga tcctcattag ggctggg   27

<210>   50
<211>   38
<212>   DNA
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<220>
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<210> 51
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<212> DNA
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<210> 52
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gactcgagga tcctcattag ggctgggcaa ggtgccttaa gacgcgg   47

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<210>   57
<211>   27
<212>   DNA
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<400>   57
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<210>   58
<211>   20
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ggtgcaattg ctcaggggag cccag                                                25


<210>   60
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<210>   61
<211>   27
<212>   DNA
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<400>   61
gactcgagga tcctcattag ggctggg                                              27


<210>   62
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<210> 63
<211> 37
<212> DNA
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ccggactggt cccgttcagg gcctgcagga gcccctg   37

<210> 64
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gaacgggacc agtccggagt tgggtcccac cttgg   35

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<212> DNA
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<210> 66
<211> 36
<212> DNA
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<400> 66
gtcgacgcta gcggcgcgcc accatggccg gacctg   36